

ES 90
ES 30

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RAW SEQUENCE LISTING

DATE: 09/09/2002

PATENT APPLICATION: US/10/050,216B

TIME: 12:50:08

Input Set : A:\CORRECTEDSEQUENCE LISTING.txt

Output Set: N:\CRF3\09092002\J050216B.raw

4 <110> APPLICANT: Curtis, Rory A.J., Lora, Jose M.
 6 <120> TITLE OF INVENTION: 46798, A Human Matrix Metalloprotease and
 7 Uses Therefore
 9 <130> FILE REFERENCE: MPI2001-014P1RNM
 11 <140> CURRENT APPLICATION NUMBER: 10/050,216B
 C--> 13 <141> CURRENT FILING DATE: 2002-08-26
 15 <150> PRIOR APPLICATION NUMBER: 60/262,252
 17 <151> PRIOR FILING DATE: 2001-01-16
 19 <160> NUMBER OF SEQ ID NOS: 10
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 2310
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (317)...(1651)
 32 <400> SEQUENCE: 1
 33 gtcgacccac gcgtccggcc gggcctccgc cccctccgccc tgcctttcct tcctccctcc 60
 34 ctcggcccc gggccggcg gaccccgcggg caggcactgc ccgggcttggc cgacgtctgg 120
 35 cccgctcccg gcgaaggggca ggggaggagc ggcccaagagc gcgcagctag ggcactggcg 180
 36 aaaccccccggg acagtccctc tccgtgcggg ggccggcgca agcagtccca tccccgggggt 240
 37 cccggggcgcg gctgactgcc ggctgggttcc ctgcgcgcag tagctccccg agccgggctg 300
 38 caccggagggc ggcgag atg gtc gcg cgc gtc ctc ctg ctg cgc gcc ctg 352
 39 Met Val Ala Arg Val Gly Leu Leu Arg Ala Leu
 40 1 5 10
 42 cag ctg cta ctg tgg ggc cac ctg gac gcc cag ccc gcg gag cgc gga 400
 43 Gln Leu Leu Leu Trp Gly His Leu Asp Ala Gln Pro Ala Glu Arg Gly
 44 15 20 25
 46 ggc cag gag ctg cgc aag gag gcg gag gca ttc cta gag aag tac gga 448
 47 Gly Gln Glu Leu Arg Lys Glu Ala Glu Ala Phe Leu Glu Lys Tyr Gly
 48 30 35 40
 50 tac ctc aat gaa cag gtc ccc aaa gct ccc acc tcc act cga ttc agc 496
 51 Tyr Leu Asn Glu Gln Val Pro Lys Ala Pro Thr Ser Thr Arg Phe Ser
 52 45 50 55 60
 54 gat gcc atc aga gcg ttt cag tgg gtg tcc cag cta cct gtc agc ggc 544
 55 Asp Ala Ile Arg Ala Phe Gln Trp Val Ser Gln Leu Pro Val Ser Gly
 56 65 70 75
 58 gtg ttg gac cgc gcc acc ctg cgc cag atg act cgt ccc cgc tgc ggg 592
 59 Val Leu Asp Arg Ala Thr Leu Arg Gln Met Thr Arg Pro Arg Cys Gly
 60 80 85 90
 62 gtt aca gat acc aac agt tat gcg gcc tgg gct gag agg atc agt gac 640
 63 Val Thr Asp Thr Asn Ser Tyr Ala Ala Trp Ala Glu Arg Ile Ser Asp

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64	95	100	105	
66	ttg ttt gct aga cac cgg acc aaa atg agg cgt aag aaa cgc ttt gca			688
67	Leu Phe Ala Arg His Arg Thr Lys Met Arg Arg Lys Lys Arg Phe Ala			
68	110	115	120	
70	aag caa ggg ggc gcc ctg gcg cac gcc ttc ctg ccc cgc cgc ggc gaa			736
71	Lys Gln Gly Gly Ala Leu Ala His Ala Phe Leu Pro Arg Arg Gly Glu			
72	125	130	135	140
74	gcg cac ttc gac caa gat gag cgc tgg tcc ctg agc cgc cgc cgg			784
75	Ala His Phe Asp Gln Asp Glu Arg Trp Ser Leu Ser Arg Arg Arg Gly			
76	145	150	155	
78	cgc aac ctg ttc gtg gtg ctg gcg cac gag atc ggt cac acg ctt ggc			832
79	Arg Asn Leu Phe Val Val Leu Ala His Glu Ile Gly His Thr Leu Gly			
80	160	165	170	
82	ctc acc cac tcg ccc gcg cgc gcg ctc atg gcg ccc tac tac aag			880
83	Leu Thr His Ser Pro Ala Pro Arg Ala Leu Met Ala Pro Tyr Tyr Lys			
84	175	180	185	
86	agg ctg ggc cgc gac gcg ctg ctc agc tgg gac gac gtg ctg gcc gtg			928
87	Arg Leu Gly Arg Asp Ala Leu Leu Ser Trp Asp Asp Val Leu Ala Val			
88	190	195	200	
90	cag agc ctg tat ggg aag ccc cta ggg ggc tca gtg gcc gtc cag ctc			976
91	Gln Ser Leu Tyr Gly Lys Pro Leu Gly Gly Ser Val Ala Val Gln Leu			
92	205	210	215	220
94	cca gga aag ctg ttc act gac ttt gag acc tgg gac tcc tac agc ccc			1024
95	Pro Gly Lys Leu Phe Thr Asp Phe Glu Thr Trp Asp Ser Tyr Ser Pro			
96	225	230	235	
98	caa gga agg cgc cct gaa acg cag ggc cct aaa tac tgc cac tct tcc			1072
99	Gln Gly Arg Arg Pro Glu Thr Gln Gly Pro Lys Tyr Cys His Ser Ser			
100	240	245	250	
102	ttc gat gcc atc act gta gac agg caa cag caa ctg tac att ttt aaa			1120
103	Phe Asp Ala Ile Thr Val Asp Arg Gln Gln Leu Tyr Ile Phe Lys			
104	255	260	265	
106	ggg agc cat ttc tgg gag gtg gca gct gat ggc aac gtc tca gag ccc			1168
107	Gly Ser His Phe Trp Glu Val Ala Ala Asp Gly Asn Val Ser Glu Pro			
108	270	275	280	
110	cgt cca ctg cag gaa aga tgg gtc ggg ctg ccc ccc aac att gag gct			1216
111	Arg Pro Leu Gln Glu Arg Trp Val Gly Leu Pro Pro Asn Ile Glu Ala			
112	285	290	295	300
114	gcg gca gtg tca ttg aat gat gga gat ttc tac ttc ttc aaa ggg ggt			1264
115	Ala Ala Val Ser Leu Asn Asp Gly Asp Phe Tyr Phe Phe Lys Gly Gly			
116	305	310	315	
118	cga tgc tgg agg ttc cgg ggc ccc aag cca gtg tgg ggt ctc cca cag			1312
119	Arg Cys Trp Arg Phe Arg Gly Pro Lys Pro Val Trp Gly Leu Pro Gln			
120	320	325	330	
122	ctg tgc cgg gca ggg ggc ctg ccc cgc cat cct gac gcc gcc ctc ttc			1360
123	Leu Cys Arg Ala Gly Gly Leu Pro Arg His Pro Asp Ala Ala Leu Phe			
124	335	340	345	
126	ttc cct cct ctg cgc cgc ctc atc ctc ttc aag ggt gcc cgc tac tac			1408
127	Phe Pro Pro Leu Arg Arg Leu Ile Leu Phe Lys Gly Ala Arg Tyr Tyr			
128	350	355	360	

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130	gtg	ctg	gcc	cga	ggg	gga	ctg	caa	gtg	gag	ccc	tac	tac	ccc	cga	agt	1456
131	Val	Leu	Ala	Arg	Gly	Gly	Leu	Gln	Val	Glu	Pro	Tyr	Tyr	Pro	Arg	Ser	
132	365				370				375						380		
134	ctg	cag	gac	tgg	gga	ggc	atc	cct	gag	gag	gtc	agc	ggc	gcc	ctg	ccg	1504
135	Leu	Gln	Asp	Trp	Gly	Gly	Ile	Pro	Glu	Glu	Val	Ser	Gly	Ala	Leu	Pro	
136							385			390					395		
138	agg	ccc	gat	ggc	tcc	atc	atc	ttc	ttc	cga	gat	gac	cgc	tac	tgg	cgc	1552
139	Arg	Pro	Asp	Gly	Ser	Ile	Ile	Phe	Phe	Arg	Asp	Asp	Arg	Tyr	Trp	Arg	
140							400			405					410		
142	ctc	gac	cag	gcc	aaa	ctg	cag	gca	acc	acc	tcg	ggc	cgc	tgg	gcc	acc	1600
143	Leu	Asp	Gln	Ala	Lys	Leu	Gln	Ala	Thr	Thr	Ser	Gly	Arg	Trp	Ala	Thr	
144							415			420					425		
146	qag	ctg	ccc	tgg	atg	ggc	tgc	tgg	cat	gcc	aac	tcg	ggg	agc	gcc	ctg	1648
147	Glu	Leu	Pro	Trp	Met	Gly	Cys	Trp	His	Ala	Asn	Ser	Gly	Ser	Ala	Leu	
148							430			435					440		
150	ttc	tgaaggcacc	tcctcaccc	agaaaactgg	ggtgctctca	gggcaaaatc											1701
151	Phe																
152	445																
154	atgttccca	ccccggggc	agaacccctc	ttagaagcct	ctgagtcct	ctgcagaaga											1761
155	ccgggcagca	aagcctccat	ctggaagtct	gtctgcctt	gttccttggaa	gaatgcagca											1821
156	ttgtctttgt	ctgtccccac	cacatggagg	tgggggtggg	atcaatctta	ggaaaagcaa											1881
157	aaaagggtcc	cagatccctt	ggccctttcc	tccgaggact	tctatccctc	ccaggcctt											1941
158	gtttcttcgg	ctaaaggta	atgttccttc	aagaggtaac	agcaactggg	tccaaagcagg											2001
159	gggatgaaa	actcagcaga	gaaattcgag	accatttgc	aagactgtgc	ccttctcctc											2061
160	aggacccct	ggctcagttc	ttgaaaaaacg	gtgtcatatt	tagtcagagg	ccccaccccc											2121
161	aggaagcatg	gatggggatg	aaggcacagg	cgtctccaa	ctcagaggcc	ctttgtgggg											2181
162	tcaggacaca	gagtgggagg	gagactgtatg	caggcttacc	agtccttgc	ttttgtctg											2241
163	gggcttggaa	aaagaggtgc	cttcagctgg	tggggccgaga	aaaaaaaaaa	aaaaaaaaaaag											2301
164	ggcggccgc																2310
166	<210>	SEQ ID NO:	2														
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168	<212>	TYPE:	PRT														
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172	Met	Val	Ala	Arg	Val	Gly	Leu	Leu	Leu	Arg	Ala	Leu	Gln	Leu	Leu	Leu	
173	1				5				10					15			
174	Trp	Gly	His	Leu	Asp	Ala	Gln	Pro	Ala	Glu	Arg	Gly	Gly	Gln	Glu	Leu	
175								20		25				30			
176	Arg	Lys	Glu	Ala	Glu	Ala	Phe	Leu	Glu	Lys	Tyr	Gly	Tyr	Leu	Asn	Glu	
177								35		40				45			
178	Gln	Val	Pro	Lys	Ala	Pro	Thr	Ser	Thr	Arg	Phe	Ser	Asp	Ala	Ile	Arg	
179								50		55				60			
180	Ala	Phe	Gln	Trp	Val	Ser	Gln	Leu	Pro	Val	Ser	Gly	Val	Leu	Asp	Arg	
181	65							70			75				80		
182	Ala	Thr	Leu	Arg	Gln	Met	Thr	Arg	Pro	Arg	Cys	Gly	Val	Thr	Asp	Thr	
183								85			90				95		
184	Asn	Ser	Tyr	Ala	Ala	Trp	Ala	Glu	Arg	Ile	Ser	Asp	Leu	Phe	Ala	Arg	
185								100		105				110			
186	His	Arg	Thr	Lys	Met	Arg	Arg	Lys	Lys	Arg	Phe	Ala	Lys	Gln	Gly	Gly	

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187 115 120 125
 188 Ala Leu Ala His Ala Phe Leu Pro Arg Arg Gly Glu Ala His Phe Asp
 189 130 135 140
 190 Gln Asp Glu Arg Trp Ser Leu Ser Arg Arg Arg Gly Arg Asn Leu Phe
 191 145 150 155 160
 192 Val Val Leu Ala His Glu Ile Gly His Thr Leu Gly Leu Thr His Ser
 193 165 170 175
 194 Pro Ala Pro Arg Ala Leu Met Ala Pro Tyr Tyr Lys Arg Leu Gly Arg
 195 180 185 190
 196 Asp Ala Leu Leu Ser Trp Asp Asp Val Leu Ala Val Gln Ser Leu Tyr
 197 195 200 205
 198 Gly Lys Pro Leu Gly Gly Ser Val Ala Val Gln Leu Pro Gly Lys Leu
 199 210 215 220
 200 Phe Thr Asp Phe Glu Thr Trp Asp Ser Tyr Ser Pro Gln Gly Arg Arg
 201 225 230 235 240
 202 Pro Glu Thr Gln Gly Pro Lys Tyr Cys His Ser Ser Phe Asp Ala Ile
 203 245 250 255
 204 Thr Val Asp Arg Gln Gln Leu Tyr Ile Phe Lys Gly Ser His Phe
 205 260 265 270
 206 Trp Glu Val Ala Ala Asp Gly Asn Val Ser Glu Pro Arg Pro Leu Gln
 207 275 280 285
 208 Glu Arg Trp Val Gly Leu Pro Pro Asn Ile Glu Ala Ala Ala Val Ser
 209 290 295 300
 210 Leu Asn Asp Gly Asp Phe Tyr Phe Lys Gly Gly Arg Cys Trp Arg
 211 305 310 315 320
 212 Phe Arg Gly Pro Lys Pro Val Trp Gly Leu Pro Gln Leu Cys Arg Ala
 213 325 330 335
 214 Gly Gly Leu Pro Arg His Pro Asp Ala Ala Leu Phe Phe Pro Pro Leu
 215 340 345 350
 216 Arg Arg Leu Ile Leu Phe Lys Gly Ala Arg Tyr Tyr Val Leu Ala Arg
 217 355 360 365
 218 Gly Gly Leu Gln Val Glu Pro Tyr Tyr Pro Arg Ser Leu Gln Asp Trp
 219 370 375 380
 220 Gly Gly Ile Pro Glu Glu Val Ser Gly Ala Leu Pro Arg Pro Asp Gly
 221 385 390 395 400
 222 Ser Ile Ile Phe Phe Arg Asp Asp Arg Tyr Trp Arg Leu Asp Gln Ala
 223 405 410 415
 224 Lys Leu Gln Ala Thr Thr Ser Gly Arg Trp Ala Thr Glu Leu Pro Trp
 225 420 425 430
 226 Met Gly Cys Trp His Ala Asn Ser Gly Ser Ala Leu Phe
 227 435 440 445
 230 <210> SEQ ID NO: 3
 231 <211> LENGTH: 1335
 232 <212> TYPE: DNA
 233 <213> ORGANISM: Homo sapiens
 235 <220> FEATURE:
 236 <221> NAME/KEY: CDS
 237 <222> LOCATION: (1)...(1335)
 239 <400> SEQUENCE: 3

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240	atg	gtc	gcg	cgc	gtc	ggc	ctc	ctg	ctg	cg	cag	ctg	cta	ctg	48		
241	Met	Val	Ala	Arg	Val	Gly	Leu	Leu	Leu	Arg	Ala	Leu	Gln	Leu	Leu		
242	1								10					15			
244	tgg	ggc	cac	ctg	gac	gcc	cag	ccc	gcc	gag	cgc	gga	ggc	cag	gag	ctg	96
245	Trp	Gly	His	Leu	Asp	Ala	Gln	Pro	Ala	Glu	Arg	Gly	Gly	Gln	Glu	Leu	
246									25					30			
248	cgc	aag	gag	gcg	gag	gca	ttc	cta	gag	aag	tac	gga	tac	ctc	aat	gaa	144
249	Arg	Lys	Glu	Ala	Glu	Ala	Phe	Leu	Glu	Lys	Tyr	Gly	Tyr	Leu	Asn	Glu	
250									40					45			
252	cag	gtc	ccc	aaa	gct	ccc	acc	tcc	act	cga	ttc	agc	gat	gcc	atc	aga	192
253	Gln	Val	Pro	Lys	Ala	Pro	Thr	Ser	Thr	Arg	Phe	Ser	Asp	Ala	Ile	Arg	
254									55					60			
256	gcg	ttt	cag	tgg	gtg	tcc	cag	cta	cct	gtc	agc	ggc	gtg	ttg	gac	cgc	240
257	Ala	Phe	Gln	Trp	Val	Ser	Gln	Leu	Pro	Val	Ser	Gly	Val	Leu	Asp	Arg	
258									70					75		80	
260	gcc	acc	ctg	cgc	cag	atg	act	cgt	ccc	cgc	tgc	ggg	gtt	aca	gat	acc	288
261	Ala	Thr	Leu	Arg	Gln	Met	Thr	Arg	Pro	Arg	Cys	Gly	Val	Thr	Asp	Thr	
262									85					90		95	
264	aac	agt	tat	gcg	gcc	tgg	gct	gag	agg	atc	agt	gac	ttg	ttt	gct	aga	336
265	Asn	Ser	Tyr	Ala	Ala	Trp	Ala	Glu	Arg	Ile	Ser	Asp	Leu	Phe	Ala	Arg	
266									100					105		110	
268	cac	cg	acc	aaa	atg	agg	cgt	aag	aaa	cgc	ttt	gca	aag	caa	ggg	ggc	384
269	His	Arg	Thr	Lys	Met	Arg	Arg	Lys	Lys	Arg	Phe	Ala	Lys	Gln	Gly	Gly	
270									115					120		125	
272	gcc	ctg	gcg	cac	gcc	ttc	ctg	ccc	cgc	cgc	gaa	g	g	cac	ttc	gac	432
273	Ala	Leu	Ala	His	Ala	Phe	Leu	Pro	Arg	Arg	Gly	Glu	Ala	His	Phe	Asp	
274									130					135		140	
276	caa	gat	gag	cg	tgg	tcc	ctg	agc	cg	cg	cg	ggg	cg	cc	ctg	ttc	480
277	Gln	Asp	Glu	Arg	Trp	Ser	Leu	Ser	Arg	Arg	Arg	Gly	Arg	Asn	Leu	Phe	
278									145					150		155	
280	gtg	gtg	ctg	gcg	cac	gag	atc	ggt	cac	acg	ctt	ggc	ctc	acc	cac	tcg	528
281	Val	Val	Leu	Ala	His	Glu	Ile	Gly	His	Thr	Leu	Gly	Leu	Thr	His	Ser	
282									165					170		175	
284	ccc	gcg	ccg	gcg	ctc	atg	gcg	ccc	tac	tac	aag	agg	ctg	ggc	cg	576	
285	Pro	Ala	Pro	Arg	Ala	Leu	Met	Ala	Pro	Tyr	Tyr	Lys	Arg	Leu	Gly	Arg	
286									180					185		190	
288	gac	gcg	ctg	ctc	agc	tgg	gac	gtg	ctg	gcc	gtg	cag	agc	ctg	tat	624	
289	Asp	Ala	Leu	Leu	Ser	Trp	Asp	Asp	Val	Leu	Ala	Val	Gln	Ser	Leu	Tyr	
290									195					200		205	
292	ggg	aag	ccc	cta	ggg	ggc	tca	gtg	gcc	gtc	cag	ctc	cca	gga	aag	ctg	672
293	Gly	Lys	Pro	Leu	Gly	Gly	Ser	Val	Ala	Val	Gln	Leu	Pro	Gly	Lys	Leu	
294									210					215		220	
296	tcc	act	gac	ttt	gag	acc	tgg	gac	tcc	tac	agc	ccc	caa	gga	agg	cg	720
297	Phe	Thr	Asp	Phe	Glu	Thr	Trp	Asp	Ser	Tyr	Ser	Pro	Gln	Gly	Arg	Arg	
298									225					230		235	
300	cct	gaa	acg	cag	ggc	cct	aaa	tac	tgc	cac	tct	tcc	tcc	gat	gcc	atc	768
301	Pro	Glu	Thr	Gln	Gly	Pro	Lys	Tyr	Cys	His	Ser	Ser	Phe	Asp	Ala	Ile	
302									245					250		255	
304	act	gta	gac	agg	caa	cag	caa	ctg	tac	att	ttt	aaa	ggg	agc	cat	ttc	816

VERIFICATION SUMMARY

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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:515 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7